

SUBSTITUTE SEQUENCE LISTING

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Rigali, Sebastien
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<120> NUCLEOTIDE AND/OR AMINO-ACID SEQUENCE
CONTROLLING THE EXPRESSION OF A XYLANASE PROMOTER-OPERATOR
NUCLEOTIDE SEQUENCE

<130> VANM201.001APC

<140> US 09/762,992

<141> 2001-02-14

<150> PCT/BE99/00105

<151> 1999-08-12

<150> US 60/096,556

<151> 1998-08-14

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 969

<212> DNA

<213> Streptomyces sp. EC3

<220>

<221> CDS

<222> (127)...(936)

<400> 1

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taggga atg	cct gct acc	gac gac cgt	cgg ccc aag	tac cag cgg	atc	168
	Met Pro Ala Thr	Asp Asp Arg Arg	Pro Lys Tyr	Gln Arg Ile		
1	5	10				

gcg gac tct	ttg cga gag	gcg atc cag	tcg ggc gag	tac ggt ccc	ggt	216
Ala Asp Ser	Leu Arg Glu	Ala Ile Gln	Ser Gly Glu	Tyr Gly Pro	Gly	
15	20	25	30			

gat cgg ctt	ccc ggg gag	aac gac ctc	atg gcc acg	cac ggc gtg	gcc	264
Asp Arg Leu	Pro Gly Glu	Asn Asp Leu	Met Ala Thr	His Gly Val	Ala	
35	40	45				

cgt atg acg	gcc cgg cag	gcg ctc ggc	gtc ctg cgg	gac gag ggc	atc	312
Arg Met Thr	Ala Arg Gln	Ala Leu Gly	Val Leu Arg	Asp Glu Gly	Ile	
50	55	60				

gcc gaa tcc	cgg aag ggc	gca ggt gtc	ttc gtg cgg	gcc ttc cgt	ccg	360
Ala Glu Ser	Arg Lys Gly	Ala Gly Val	Phe Val Arg	Ala Phe Arg	Pro	

65	70	75	
ctg cgc cga cgc ggc atc cag cgg ctg gcc cgc gac cag tgg ggc aac			408
Leu Arg Arg Arg Gly Ile Gln Arg Leu Ala Arg Asp Gln Trp Gly Asn			
80	85	90	
gga cgg tcc atc tgg tcg gcg gac atc gag gcc aga gac ctc cgg gtc			456
Gly Arg Ser Ile Trp Ser Ala Asp Ile Glu Ala Arg Asp Leu Arg Val			
95	100	105	110
gac cag gtc tcg gtg ggc gag gag aaa gct ccc gag cac atc ggc gcg			504
Asp Gln Val Ser Val Gly Glu Glu Lys Ala Pro Glu His Ile Gly Ala			
115	120	125	
gtc ctg ggc atg gct gcc gaa gaa gtc gcg tgc gtg agg cgc cgg cgc			552
Val Leu Gly Met Ala Ala Glu Glu Val Ala Cys Val Arg Arg Arg			
130	135	140	
ttc gtc ctg gac ggc aag ccg gtg ctg ctc gcg acg agt tac ctg ccc			600
Phe Val Leu Asp Gly Lys Pro Val Leu Leu Ala Thr Ser Tyr Leu Pro			
145	150	155	
ctg tcc ctg gtg gcc gga tcc gcc atc agc cga gag gac acc ggg ccg			648
Leu Ser Leu Val Ala Gly Ser Ala Ile Ser Arg Glu Asp Thr Gly Pro			
160	165	170	
ggc ggt acc tac gcc cgg ctt gcc gaa ctc ggc cac gaa ccg gtg cac			696
Gly Gly Thr Tyr Ala Arg Leu Ala Glu Leu Gly His Glu Pro Val His			
175	180	185	190
ttc cgc gag gag atc cgc tca cgc atg ccg tcg ccg gac gag gtg aca			744
Phe Arg Glu Glu Ile Arg Ser Arg Met Pro Ser Pro Asp Glu Val Thr			
195	200	205	
cag ctg gac ctt gcc ccg ggc acc ccg gtc atc ctc atc tgc cgc acc			792
Gln Leu Asp Leu Ala Pro Gly Thr Pro Val Ile Leu Ile Cys Arg Thr			
210	215	220	
gcg ttc acc gac cag ggc cac cct gtc gag gtc aac gag atg acc ctg			840
Ala Phe Thr Asp Gln Gly His Pro Val Glu Val Asn Glu Met Thr Leu			
225	230	235	
gac gcc gct tcc tac gtc ttg gag tac gac ttc gac gcg ggc ccc gag			888
Asp Ala Ala Ser Tyr Val Leu Glu Tyr Asp Phe Asp Ala Gly Pro Glu			
240	245	250	
ccc gcc tcc ccc ggc gcc gac gcc aca gcg ccc gga gac ccg gcc tga			936
Pro Ala Ser Pro Gly Ala Asp Ala Thr Ala Pro Gly Asp Pro Ala *			
255	260	265	
cagcgggcga ccgttggaag tcctcgcatc ccg			969
<210> 2			
<211> 269			
<212> PRT			
<213> Streptomyces sp. EC3			
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 Ser Leu Arg Glu Ala Ile Gln Ser Gly Glu Tyr Gly Pro Gly Asp Arg
 20 25 30
 Leu Pro Gly Glu Asn Asp Leu Met Ala Thr His Gly Val Ala Arg Met
 35 40 45
 Thr Ala Arg Gln Ala Leu Gly Val Leu Arg Asp Glu Gly Ile Ala Glu
 50 55 60
 Ser Arg Lys Gly Ala Gly Val Phe Val Arg Ala Phe Arg Pro Leu Arg
 65 70 75 80
 Arg Arg Gly Ile Gln Arg Leu Ala Arg Asp Gln Trp Gly Asn Gly Arg
 85 90 95
 Ser Ile Trp Ser Ala Asp Ile Glu Ala Arg Asp Leu Arg Val Asp Gln
 100 105 110
 Val Ser Val Gly Glu Glu Lys Ala Pro Glu His Ile Gly Ala Val Leu
 115 120 125
 Gly Met Ala Ala Glu Glu Val Ala Cys Val Arg Arg Arg Phe Val
 130 135 140
 Leu Asp Gly Lys Pro Val Leu Leu Ala Thr Ser Tyr Leu Pro Leu Ser
 145 150 155 160
 Leu Val Ala Gly Ser Ala Ile Ser Arg Glu Asp Thr Gly Pro Gly Gly
 165 170 175
 Thr Tyr Ala Arg Leu Ala Glu Leu Gly His Glu Pro Val His Phe Arg
 180 185 190
 Glu Glu Ile Arg Ser Arg Met Pro Ser Pro Asp Glu Val Thr Gln Leu
 195 200 205
 Asp Leu Ala Pro Gly Thr Pro Val Ile Leu Ile Cys Arg Thr Ala Phe
 210 215 220
 Thr Asp Gln Gly His Pro Val Glu Val Asn Glu Met Thr Leu Asp Ala
 225 230 235 240
 Ala Ser Tyr Val Leu Glu Tyr Asp Phe Asp Ala Gly Pro Glu Pro Ala
 245 250 255
 Ser Pro Gly Ala Asp Ala Thr Ala Pro Gly Asp Pro Ala
 260 265

<210> 3
 <211> 195
 <212> DNA
 <213> Streptomyces sp. EC3

<400> 3
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 cccggtgatc ggcttcccg ggagaacgac ctcatggcca cgcacggcgt ggcccgtatg 120
 acggcccggc aggcgctcgg cgtcctgcgg gacgagggca tcgccgaatc ccggaagggc 180
 gcaggtgtct tcgtg 195

<210> 4
 <211> 137
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> polylinker

<400> 4
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cggtaccagg cctaatt 137

<210> 5
 <211> 133
 <212> DNA
 <213> Streptomyces sp. EC3

<400> 5
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 cagaagctta atattttaatt aagcggccgc agtactctcg agccgccatg ggcccgatat 120
 cggtaccagg cct 133

<210> 6
 <211> 12
 <212> DNA
 <213> Streptomyces sp. EC3

<400> 6
 cgaaactggt ga 12

<210> 7
 <211> 16
 <212> DNA
 <213> Streptomyces sp. EC3

<400> 7
 tttccgaaag tttgcc 16

<210> 8
 <211> 12
 <212> DNA
 <213> Streptomyces sp. EC3

<400> 8
 tcgaaacttt cg 12

<210> 9
 <211> 15
 <212> DNA
 <213> Streptomyces sp. EC3

<220>
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 <222> (1)...(15)
 <223> n = A,T,C or G

<400> 9
 tnncgaaann gncnc 15